AMENDMENTS TO THE SPECIFICATION

On page 25, replace the paragraph starting on line 26 with the following:

After isolating the *Hunk* kinase (Example 1) and cloning and characterizing *Hunk* as a novel member of the family of SNF1-related protein kinases (Example 2), four founder mice were identified in Example 3 as harboring the MMTV-*Hunk* transgene in DNA that passed the transgene to offspring in a Mendelian fashion. When screened for transgene expression by Northern hybridization and RNase protection analysis, one [[. One]] founder line, MHK3, was identified that expressed the MMTV-*Hunk* transgene at high levels, and it became the focus of comparisons with endogenous *Hunk* expression during all stages of postnatal mammary development.

On page 48, replace the paragraph starting on line 3 with the following:

RNase protection analysis. FIG. 5A depicts an RNase protection analysis of *Hunk* mRNA spacial expression in tissues of the adult mouse. 30 μg of RNA isolated from the indicated murine tissues was hybridized with antisense RNA probes specific for *Hunk* and for *β-actin*. Ribonuclease protection analysis was performed as described (Marquis *et al.*, 1995). Body-labeled anti-sense riboprobes were generated using linearized plasmids containing nucleotides 276 to 500 of the *Hunk* cDNA and 1142 to 1241 of *β-actin* (GenBank Accession No. X03672) using [α-^{32}P]UTP and the Promega *in vitro* transcription system with T7 polymerase. The β-actin antisense riboprobe was added to each reaction as an internal control. Probes were hybridized with RNA samples at 58°C overnight in 50% formamide/100 mM Pipes ~~[define]~~ (pH 6.7). Hybridized samples were digested with RNase A and T1, purified, electrophoresed on a 6% denaturing polyacrylamide gel, and subjected to autoradiography.

On p. 50, replace the paragraph starting on line 27 with the following:

No recombinants were detected between *Hunk* and *Tiam1* in 130 animals typed in common, suggesting that the two loci are within 2.3 cM of each other (upper 95% confidence limit). When the interspecific map of chromosome 16 was compared with a composite mouse linkage map that reports the map location of many uncloned mouse mutations (at ~~http://~~ www.informatics.jax.org [[/]]), *Hunk* mapped in a region of the composite map that lacks mouse mutations (data not shown).